

20200926001

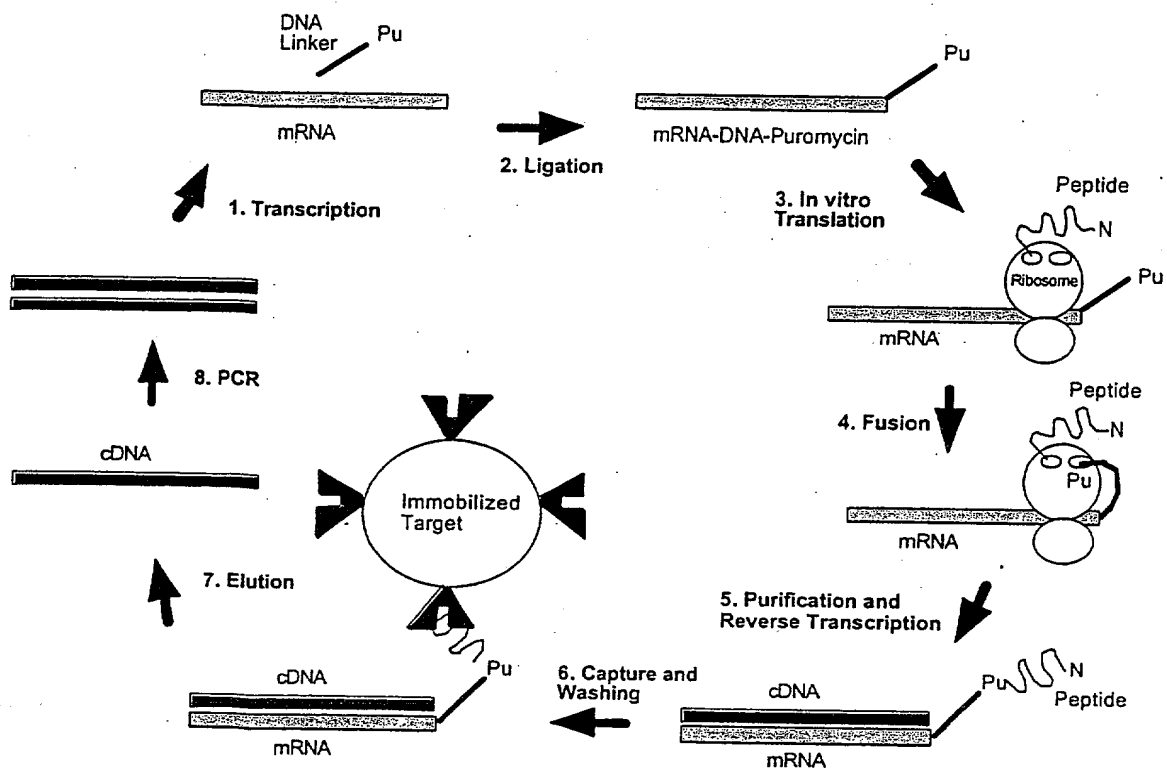


FIGURE 1

A.

Bcl-2										M	P	V	V	H	L	T	L	T	T	A	G	D	D	F	S	R	R
Bax	M	P	Q	D	A	S	T	K	K	L	S	E	C	L	K	R	I	G	D	E	L	D	S	N	G		
Bak											M	G	Q	V	G	R	Q	L	A	I	I	G	D	D	I	N	

B.

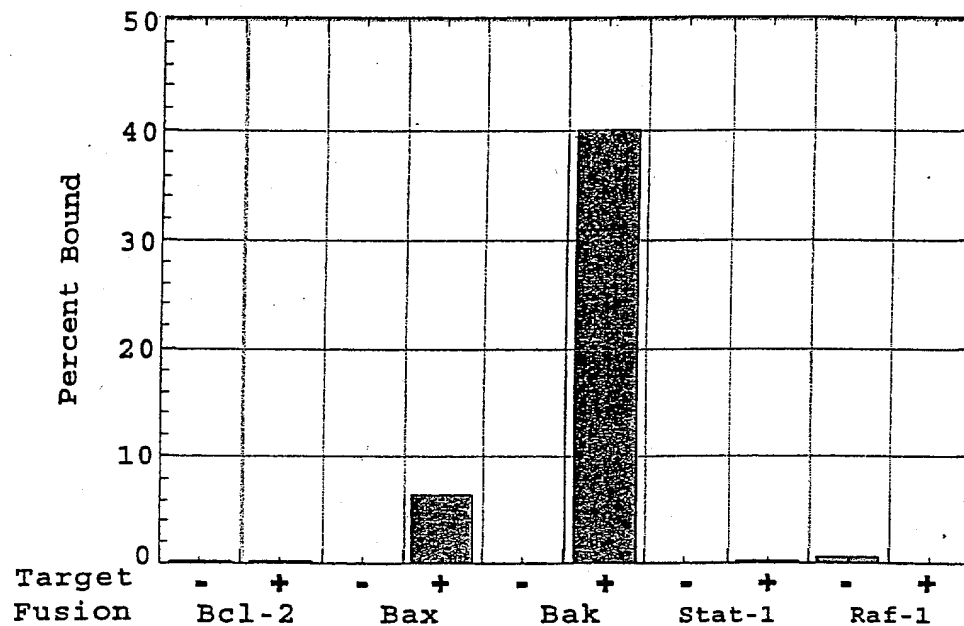


FIGURE 2

20200909-0922600T

Number	Protein Name	Accession numbers	Clone	Protein Sequence	Kd	R value	GST Binding Percent	Bal:PH3 [uM]	Bal:PH3 effect	Kidney	Liver	Marrow	Total
1	Bim	NP 006529.1	144	ASMRQAEPAADMRPEWIAQELRRIGDEFNAYARE	0.0019	0.97	0.3	100	0.84	42	11	36	89
2	Bak	NP 001179.1	C32	GVGRGLAIGDINRRK	0.0019	0.98	0.2	100	0.36	2	2	1	5
3	Bax	NP 004315.1	C49	KLSECLRRIGDELSEAEVQINQKADSPALRSKLVRLSSDSFAHL	0.76	0.98	1.1	20	0.06	19	0	0	19
4	Bcl2 L12	AF299230.1	W75	TGKALRLRLLVALLCEAEVQINQKADSPALRSKLVRLSSDSFAHL	0.00416	0.99	0.4	20	0.66	0	0	0	0
5	Neurophilin cytosolic factor 2	NP 004024.1	192	GRGMLYQTEKQDALKLQKALQLRGNN	0.0093	0.98	0.8	20	0.21	0	0	0	0
6	Talin (splice variant)	NP 002480.1	156	GGESDTPDFQDALQKAAVAAAALVAKKSAQR	0.467	0.94	0.1	20	0.21	4	0	0	4
7	Golgi SNAP receptor complex member 1	NP 004862.1	W06	GTRDMFQREIHQAEIOLALRTGVNDKMAEYVINA	0.58	0.97	0.8	20	0.21	9	13	11	35
8	HSCP300	AF161418	658	AVQDPVQREIHQAEIOLALRTGVNDKMAEYVINA	0.64	0.88	1.4	20	0.14	8	4	0	12
9	Syntaxin 4A	NP 004595.1	U58	ATQALNLSHPSHGQCLEVGRSIRHLEDFTL	0.69	0.98	1.3	20	0.18	1	5	0	6
10	Tumor protein HDMC21P	NP 003236.1	U50	WFSVQVREIAGQCLEVGRSIRHLEDFTL	0.781	0.98	0.5	20	0.32	4	0	0	4
11	Toll-like receptor 3	NP 003236.1	U50	WFSVQVREIAGQCLEVGRSIRHLEDFTL	1.12	0.95	0.3	20	0.07	0	0	0	0
12	Voltage dependent anion channel 3	NP 005653.1	W06	WFSVQVREIAGQCLEVGRSIRHLEDFTL	2.5	0.99	0.1	20	0.1	3	0	1	4
13	Aldehyde dehydrogenase	P06847	U57	IGTAPRQVQVQATKVLNRNADFNVDRLP	2.75	0.99	0.2	20	0.08	0	0	0	0
14	Human reticulospinal L1	NP 003283.1	U57	IGTAPRQVQVQATKVLNRNADFNVDRLP	4.25	0.97	1.5	20	0.16	23	0	1	24
15	TPR, nuclear pore complex-associated protein	NP 005653.1	U57	IGTAPRQVQVQATKVLNRNADFNVDRLP	4.46	0.97	1.5	20	0.09	5	0	0	5
16	TRAP100 Thyroid hormone receptor-associated protein	AAC39855.1	U25	TYNLLPPRPIKEVLDITAKVLEKGVWDSSRS	5.24	0.88	0.3	20	0.19	1	1	0	2
17	Parathyroid hormone receptor	NM_000316.1	U56	LFTILLTLTWTHCSTPSG	7.24	0.92	0.4	20	0.08	1	3	0	4
18	Calpain	P07384	U53	AGEOMEISVKEATILNRISIKKOLRT	8.9	0.89	0.2	100	0	1	1	0	2
19	Occludin, tight junction protein	NP 002529.1	X33	GLRESESEYMAADEYNRLKQVAKPA	9.6	0.91	0.2	20	0.02	0	0	0	0
20	Human nGAP protein	NP 004832.1	C26	KGIISRLSVSEELKHDHWAEMAGCGLTQEDHLMPPRSFAFSLDAVNARLMSALTIPAXRVVXHCX	PD	0.91	0.2	20	0.5	3	0	0	3
21	Ankyrin 2	NP 001139.2	X69	WERIEERLVAIEDHGLFSTELARAL	PD	0.91	0.2	20	0.27	0	0	0	0
22	Skeletal regulatory element binding tm factor (splice)	NP 004167.2	W17	ARGDFAQAQQQLWALRALRKPPLPTSH	PD	0.91	0.2	20	0.31	0	0	0	0
23	Diazotrophic kinase Zeta	NP 003637.1	W49	GSSKQAKHQVQCDGMILTPKPHDLKPPQC	PD	0.91	0.2	20	0.21	1	1	0	2
24	Transferrin	NP 004613.1	C08	GFLAAEQDIREIRKVVQSLQEQTAREVLTLLQ	PD	0.95	1.4	20	0.79	1	1	0	2
25	Fig. C associated interferon-induced microtubular	NP 006408.1	U53	LDPVKDLISALRRMAAADDLEDFLFFQIG	5.04	0.95	1.4	20	0.36	0	0	0	0
26	Mitochondrial NADH dehydrogenase subunit 1	NP 008342.1	U57	ANLLMLPILLIAMFLMTERKILGYIQPR	PD	0.95	1.4	20	0.36	0	0	0	0
27	Mitochondrial ATP synthase FO sector 8	NP 008346.1	C54	LRNLTVPITPILTLFLTNRLITTR	PD	0.95	1.4	20	0.36	0	0	0	0
28	Mitochondrial NADH dehydrogenase subunit 5	NP 008352.1	C46	AGVSAEAPFPQRRSMVFARHLREVQDEFRRSLHSTDDADE	4.95	0.92	0.6	20	0.21	1	1	0	2
29	Hypothetical protein DN724643.1	T14795	X68	MRDLPVGHYETKLVGHKLTADHR	PD	0.92	0.6	20	0.21	1	1	0	2
30	Hypothetical protein DN724643.1	T14795	X68	MRDLPVGHYETKLVGHKLTADHR	PD	0.92	0.6	20	0.21	1	1	0	2
31	Hypothetical protein DN724643.1	T14795	X68	MRDLPVGHYETKLVGHKLTADHR	PD	0.92	0.6	20	0.21	1	1	0	2
32	Hypothetical protein DN724643.1	T14795	X68	MRDLPVGHYETKLVGHKLTADHR	PD	0.92	0.6	20	0.21	1	1	0	2
33	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
34	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
35	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
36	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
37	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
38	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
39	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
40	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
41	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
42	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
43	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
44	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
45	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
46	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
47	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
48	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
49	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
50	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
51	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
52	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
53	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
54	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
55	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
56	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
57	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
58	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
59	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
60	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
61	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
62	Unknown protein from Homo sapiens cDNA: FL224	AK009344.1	X37	CGGMRDIPGSRGVGHKYPKVPKAGVSLARNLRVADWM	0.0129	0.9	0.4	20	0.36	0	0	0	0
63	Proline/glutamine rich splicing factor (out of frame)	NM_005066	C83	RLGVDRVLEWGLLEPRO	PD	0.87	4.2	20	0.36	0	0	0	0
64	Transforming growth factor (reversed orientation)	NM_003758	X84	FYRSVGVWALQDDMDHAIQCHDVRLG	PD	0.87	4.2	20	0.36	0	0	0	0
65	Lipid transfer protein	NM_002298	X91	AGTQPLIAQFMRVGGDELLHFLW	PD	0.87	4.2	20	0.36	0	0	0	0
66	Arsenate resistance protein (reversed orientation)	NM_015908	X91	MDTKGDLITNFQVADALNLSLLPPLATA	PD	0.87	4.2	20	0.36	0	0	0	0
67	K-Ras oncogene (3' UTR)	NM_004985	C1	ATWKTQGLLDRIQAPSPSPH	PD	0.87	4.2	20	0.36	0	0	0	0
68	Lysosomal peptidase insensitive protease (3' UTR)	AF039704	C41	ENARKQPKPNSSSTAYNFTGVSLPSYAP	PD	0.87	4.2	20	0.36	0	0	0	0
69	MYBPC3 (3' UTR)	NM_000256	C4	GSLLTHNNIKPSSR	PD	0.87	4.2	20	0.36	0	0	0	0
70	CDNA FL20617 (not in predicted ORF)	AK006624	C4	VSCWPSYKPLSTASLASLATQLKXIA	PD	0.87	4.2	20	0.36	0	0	0	0
71	CDNA FL20617 (not in predicted ORF)	AK006624	C4	VSCWPSYKPLSTASLASLATQLKXIA	PD	0.87	4.2	20	0.36	0	0	0	0

FIGURE 3B

SEQ ID NO 1: BimL (Corresponds to the nucleic acid sequence of SEQ ID NO: 153)
A S M R Q A E P A D M R P E I W I A Q E L R R I G D E F N A Y Y A R E

SEQ ID NO: 2 Bak (Corresponds to the nucleic acid sequence of SEQ ID NO: 154)
G Q V G R Q L A I I G D D I N R R K

SEQ ID NO: 3 Bax (Corresponds to the nucleic acid sequence of SEQ ID NO: 155)
K L S E C L K R I G D E L D S N M E L Q R M I A A V D T D S P R

SEQ ID NO: 4 Bcl2 L12 (Corresponds to the nucleic acid sequence of SEQ ID NO: 156)
T G K E A I L R R L V A L L E E E A E V I N Q K L A S D P A L R S K L V R L S S D S F A
H L

SEQ ID NO: 5 Neutrophil cytosolic factor 2 (Corresponds to the nucleic acid sequence of SEQ ID NO: 157)
Q R G M L Y Y Q T E K Y D L A I K D L K E A L I Q L R G N N

SEQ ID NO: 6 Talin (splice variant) (Corresponds to the nucleic acid sequence of SEQ ID NO: 158)
G G E S D T D P H F Q D A L M Q L A K A V A S A A A A L V L K A K S V A Q R

SEQ ID NO: 7 Golgi SNAP receptor complex member 1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 159)
G T R Q D R M F E T M A I E I E Q L L A R L T G V N D K M A E Y T N A

SEQ ID NO: 8 HSCP300 (Corresponds to the nucleic acid sequence of SEQ ID NO: 160)
A V Q E D P V Q R E I H Q D W A N R E Y I E I T S S I K K I A D

SEQ ID NO: 9 Syntaxin 4A (Corresponds to the nucleic acid sequence of SEQ ID NO: 161)
A T R Q A L N E I S A R H S G I Q Q L E R S I R E L H D I F T F L

SEQ ID NO: 10 Tumor protein HDCMB21P (Corresponds to the nucleic acid sequence of SEQ ID NO: 162)
M F S D I Y G I R E I A D G L C L E V E G K M V S R P E

SEQ ID NO: 11 Toll-like receptor 3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 163)
F W L E E R D F E A G V F E L E A I V N S I K R S

SEQ ID NO: 12 Voltage dependent anion channel 3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 164)
M K W D T D N T L G T E I S W E N K L A E G L K L T L D T I F V H H V L H A P H

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FIGURE 3B

SEQ ID NO: 13 Aldehyde dehydrogenase (Corresponds to the nucleic acid sequence of SEQ ID NO: 165)

R G A V F S Q D K D V V Q E A T K V L R N A A D N F Y I N D R

SEQ ID NO: 14 Human retrotransposon L1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 166)

T G T G A P R F I K E V Q E L N S A L H Q S D L I D I Y R T L H P

SEQ ID NO: 15 TPR, nuclear pore complex-associated protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 167)

S N E L T R A V E E L H K L L K E A R E

SEQ ID NO: 16 TRAP100 Thyroid hormone receptor-associated protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 168)

T Y W N L L P P K R P I K E V L T D I F A K V L E K G W V D S R S

SEQ ID NO: 17 Parathyroid hormone receptor (Corresponds to the nucleic acid sequence of SEQ ID NO: 169)

L F T I L L T L W T M R C S S T P S G

SEQ ID NO: 18 Calpain (Corresponds to the nucleic acid sequence of SEQ ID NO: 170)

A G E D M E I S V K E L R T I L N R I I S K H K D L R T

SEQ ID NO: 19 Occludin, tight junction protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 171)

G L R E E S E E Y M A A A D E Y N R L K Q V K Q P A

SEQ ID NO: 20 Human nGAP protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 172)

K G I I S R L M S V E E E L K R D H A E M Q A G C G L Q T E D H L M P R R S A F A S L
D A V N A R L M S A L T P A X R Y V X H C X P L

SEQ ID NO: 21 Ankryn 2 (Corresponds to the nucleic acid sequence of SEQ ID NO: 173)

W E R I E E R L A Y I A D H L G F S W T E L A R A L

SEQ ID NO: 22 Sterol regulatory element binding txn factor (splice variant) (Corresponds to the nucleic acid sequence of SEQ ID NO: 174)

A R G D F A Q A A Q Q L W L A L R A L G R P L P T S H

SEQ ID NO: 23 Diacylglycerol kinase Zeta (Corresponds to the nucleic acid sequence of SEQ ID NO: 175)

G S S K D L A K H I Q V V C D G M D L T P K I H D L K P Q C

FIGURE 3B

SEQ ID NO: 24 Translin (Corresponds to the nucleic acid sequence of SEQ ID NO: 176)
GFLAAEQDIREERKVVQSLEQTAREVLTLLQG

SEQ ID NO: 25 Hep C associated,interferon-induced microtubular (Corresponds to the nucleic acid sequence of SEQ ID NO: 177)
LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG

SEQ ID NO: 26 Mitochondrial NADH dehydrogenase subunit 1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 178)
ANLLLLMVPILIAMAFMLTERKILGYIQPR

SEQ ID NO: 27 Mitochondrial ATP synthase F0 subunit 8 (Corresponds to the nucleic acid sequence of SEQ ID NO: 179)
LRLNTTVWPTIITPILLTLFLITNRLITTR

SEQ ID NO: 28 Mitochondrial NADH dehydrogenase chain 5 (Corresponds to the nucleic acid sequence of SEQ ID NO: 180)
TLYLKLTALAVTFLGLLTALDLNYPT

SEQ ID NO: 29 Hypothetical protein DFKZp434e171 (Corresponds to the nucleic acid sequence of SEQ ID NO: 181)
AGVFS AEPSPFPQTRRSMVFARHLREVGDEFRRHLNSTDDAD
E

SEQ ID NO: 30 Hypothetical protein DKFZp566f2124 (Corresponds to the nucleic acid sequence of SEQ ID NO: 182)
GLKLATVAASMDRVPKVTPSSAIISSIARENHEPERLGLNGIAET
T

SEQ ID NO: 31 Hypothetical protein KIAA1501 (Corresponds to the nucleic acid sequence of SEQ ID NO: 183)
MRDLPGHYEYETLKFLVGHLKTIADHR

SEQ ID NO: 32 Hypothetical protein DKFZp586ho623 (Corresponds to the nucleic acid sequence of SEQ ID NO: 184)
CGGRMEDIPCSRVGHIYRKYPYKVPAGVSLARNLKRVDWM

SEQ ID NO: 33 unknown protein from cDNA: FLJ21691 fis, clone COL09555 (Corresponds to the nucleic acid sequence of SEQ ID NO: 185)
ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLC AHP

FIGURE 3B

SEQ ID NO: 34 unknown protein from Mitochondrial DNA (Corresponds to the nucleic acid sequence of SEQ ID NO: 186)

TSTLPHIRRTR

SEQ ID NO: 35 Unknown protein from Homo sapiens cDNA: FLJ23277 fis, clone HEP03322 (Corresponds to the nucleic acid sequence of SEQ ID NO: 187)

NGNLFASFADS

SEQ ID NO: 36 unknown protein from Homo sapiens cDNA: FLJ22171 fis, clone HRC00654 (Corresponds to the nucleic acid sequence of SEQ ID NO: 188)

ILTSPWTTSSGLWPRLQKAAEAFKQLNQP

SEQ ID NO: 37 unknown protein from cDNA FLJ23179 fis, clone LNG10890 (Corresponds to the nucleic acid sequence of SEQ ID NO: 189)

RTLQPRLQLNQQQHLPALPIWFLLQWLRLHPL

SEQ ID NO: 38 unknown protein from clone RP5-889J22 on chromosome 22q13.1 (Corresponds to the nucleic acid sequence of SEQ ID NO: 190)

MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSTP

SEQ ID NO: 39 Unknown protein from Mitochondrial DNA (Corresponds to the nucleic acid sequence of SEQ ID NO: 191)

GLAKKSKRNPANLTPP

SEQ ID NO: 40 Unknown protein from Homo sapiens chromosome X (Corresponds to the nucleic acid sequence of SEQ ID NO: 192)

SSQALRIHQWLHLFSDFTST

SEQ ID NO: 41 unknown protein bfrom clone RP11-141E20 on chromosome 1q31.2-31.3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 193)

GQVGRQLAIIIGDDINRRK

SEQ ID NO: 42 unknown protein from chromosome 21q22.2, cosmid clone:D37D12, CBR1-HLCS region (Corresponds to the nucleic acid sequence of SEQ ID NO: 194)

GVSEAEGETFPLSTFLLGIASRLRSVA

SEQ ID NO: 43 Unknown protein from Homo sapiens clone RP11-198M19, homology to retrotransposon (Corresponds to the nucleic acid sequence of SEQ ID NO: 195)

RAPRFIKQILLDLKREIDFNVRLEVEYFNPLS

FIGURE 3B

SEQ ID NO: 44 Unknown protein with RNA Homology to Murine retrovirus readthrough seq.
(Corresponds to the nucleic acid sequence of SEQ ID NO: 196)

I V A I I A G R L R M L G D Q F N G E L E A S A K N

SEQ ID NO: 45 Unknown protein from CpG island (Corresponds to the nucleic acid sequence
of SEQ ID NO: 197)

L A L A Y Y S S R Q Y A S A L K H I A E I I E R G I R Q H

SEQ ID NO: 46 unknown protein from clone 425C14 on chromosome 6q22 (Corresponds to the
nucleic acid sequence of SEQ ID NO: 198)

A A M L L D R R G T E C D L W I N E M S L L H K I V Q D V Y G T P H P P H S

SEQ ID NO: 47 unknown protein from Human genomic DNA of Xq28 with MTM1 and
MTMR1 genes (Corresponds to the nucleic acid sequence of SEQ ID NO: 199)

P W Q Y K P I A D L Y R G R E S R P S A P R

SEQ ID NO: 48 unknown protein from clone RP11-517O1 on chromosome X (Corresponds to
the nucleic acid sequence of SEQ ID NO: 200)

L F S V L L R Y L A D N F L P G G S

SEQ ID NO: 49 Unknown protein from PAC clone RP5-1021I20 from 14q24.3 (Corresponds to
the nucleic acid sequence of SEQ ID NO: 201)

D W Q V L L G K L L W K I D N P G I

SEQ ID NO: 50 unknown protein from in DNA of chromosomes 8, 10, 14, 16 (Corresponds to
the nucleic acid sequence of SEQ ID NO: 202)

G A M E R E W A M F L R A A S S R I R G G V

SEQ ID NO: 51 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 203)

V H N F G R H W G L P L S F L L N Y P L F L S P

SEQ ID NO: 52 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 204)

A S M A P V G R D A E T L Q K Q K E T I K A F L K K L E A L M A S N D N A N K T

SEQ ID NO: 53 Sequence/protein not in database (Corresponds to the nucleic acid sequence of
SEQ ID NO: 205)

C R E Q A E L T G L R L A S L G L K F N K I V H S S M T R A I E T

FIGURE 3B

SEQ ID NO: 54 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 206)

GTRISDMLKLIADTWQRNCCPA

SEQ ID NO: 55 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 207)

EQASVKYVILDMYRALLTLMNTSTAT

SEQ ID NO: 56 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 208)

EDLESVLIRLINWAKGSPIP

SEQ ID NO: 57 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 209)

RPVSFCGAVWTLNRAIGRHFVRGSR

SEQ ID NO: 58 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 210)

HAVVARLLHIGAIMEFQRLDFIEQLSAPPA

SEQ ID NO: 59 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 211)

GQGT LWGSGMEAWLATVLKALPWHPTYQLEP

SEQ ID NO: 60 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 212)

IAQATKATIDKWNCIKLKIFYTSKKEAS

SEQ ID NO: 61 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 213)

VVDVPDFIVWLEEA VSDLHRAL

SEQ ID NO: 62 Sequence/protein not in database (Corresponds to the nucleic acid sequence of SEQ ID NO: 214)

QRRGNEFQLRDLADAWDLSSRSRQRGWQMPNCRSRRGPG

SEQ ID NO: 63 Proline/glutamine rich splicing factor (Corresponds to the nucleic acid sequence of SEQ ID NO: 215)

RGLWVDRVLEEWGLEPRQ

FIGURE 3B

SEQ ID NO: 64 Transforming growth factor (Corresponds to the nucleic acid sequence of SEQ ID NO: 216)

FVRSVGVRLQNIGDDMDHAICGHDVRLG

SEQ ID NO: 65 L-plastin (Corresponds to the nucleic acid sequence of SEQ ID NO: 217)

--SGLRKPTCGSSQR

SEQ ID NO: 66 Arsenate resistance protein (Corresponds to the nucleic acid sequence of SEQ ID NO: 218)

AGTQPLILAQFMRVGGDELLHFLLW

SEQ ID NO: 67 K-Ras oncogene (Corresponds to the nucleic acid sequence of SEQ ID NO: 219)

MDTIKGFDLITNFQVVADALNISLLPNPLATA

SEQ ID NO: 68 Lysosomal pepstatin insensitive protease (Corresponds to the nucleic acid sequence of SEQ ID NO: 220)

ATWMKTLQGLLDRIQAFPSSPH

SEQ ID NO: 69 MYBPC3 (Corresponds to the nucleic acid sequence of SEQ ID NO: 221)

EANRKQPKPNNSSTAYYNFTGVSILPSYKP

SEQ ID NO: 70 cDNA FLJ20617 (Corresponds to the nucleic acid sequence of SEQ ID NO: 222)

GSLTHHINNIKPSSTR

SEQ ID NO: 71 UDP glucuronosyl transferase 2B4 precursor (Corresponds to the nucleic acid sequence of SEQ ID NO: 223)

VSCWPSYLKYPLSTASASLLATQLKSIA

FIGURE 3C

SEQ ID NOS:72 and 153

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGCTTCCATGA
GGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTG
GAGACGAGTTTAAACGCCTACTATGCAAGGGAGGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

SEQ ID NOS:73 and 154

TACTATTTACAATTCTCCTAACACAATGGGGGCAGGTGGGGACGGCAGCTCGCCATCATCGGG
GACGACATCAACCGACGGAAAGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAAA

SEQ ID NOS:74 and 155

TTTACAATTCTCCTAACACAATGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGAACTGG
ACAGTAACATGGAGCTGCAGAGGATGATTGCCGCCGTGGACACAGACTCCCCCGAGATTACA
AAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:75 and 156

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTCTCTACAATGACAGGGAAGG
AAGCCATACTGCGGAGGCTGGTGGCCCTGCTGGAGGAGGAGGCAGAAGTCATTAACCAGAAGC
TGGCCTCGGACCCCGCCCTGCGCAGCAAGCTGGTCCGCCCTGTCTCCGACTCTTTCGCCCACC
TGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:76 and 157

GACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCCAACGAGGGATGCTCTACTACC
AGACAGAGAAATATGATTTGGCTATCAAAGACCTTAAAGAAGCCTTGATTGAGCTTCGAGGGA
ACAATGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:77 and 158

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGGTGGGGAAA
GTGATACTGACCCCCACTTCCAGGATGCGCTAATGCAGCTCGCCAAAGCTGTGGCAAGTGCTG
CAGCTGCCCTGGTCTCAAGGCCAAGAGTGTGGCCCAACGAGATTACAAAGACGATGACGATA
GGGCATCCGCTATTTAAAA

SEQ ID NOS:78 and 159

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTCTCTACAATGGGAACACGCC
AAGACAGAATGTTTGAGACAATGGCGATTGAGATTGAACAACCTTTGGCAAGGCTTACAGGGG
TAAATGATAAAATGGCAGAATATACCAACGCTGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

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FIGURE 3C

SEQ ID NOS:79 and 160

CTATTTACAATTCTCCTAACACAATGGCGGTACAGGAGGATCCGGTGCAGCGGGAGATTCACC
AGGACTGGGCTAACCGGGAGTACATTGAGATAATCACCAGCAGCATCAAGAAAATCGCAGACT
TTCTCAACTCGTTCGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:80 and 161

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGCGACTCGAC
AGGCCTTAAATGAGATCTCGGCCCGGCACAGTGGGATCCAGCAGCTTGAACGCAGTATTCGTG
AGCTGCACGACATATTCACTTTTCTGGCTACCGAAGTGCGAGATTACAAAGACGATGACGATA
AGGCATCCGCTATTAAAAA

SEQ ID NOS:81 and 162

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGATGTTCTCCG
ACATCTACGGGATCCGGGAGATCGCGGACGGGTTGTGCCTGGAGGTGGAGGGGAAGATGGTCA
GTAGGCCAGAGGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:82 and 163

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGTTTTGGCTGG
AAGAAAGGGACTTTGAGGCGGGTGTTTTTGAAGTAGAAGCAATTGTTAACAGCATCAAAAGAA
GCGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:83 and 164

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCAATACAATGAAATGGG
ACACAGACAATACTCTAGGGACAGAAATCTCTTGGGAGAATAAGTTGGCTGAAGGGTTGAAAC
TGACTCTTGATACCATATTTGTACATCACGTCTGCATGCCCCACACGATTACAAAGACGATG
ACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:84 and 165

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCGGGGGGCAG
TGTTCTCCCAGGATAAGGACGTCGTGCAGGAGGCCACAAAGGTGCTGAGGAATGCTGCCGACA
ACTTCTACATCAACGACAGGGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:85 and 166

GACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGACCGGTACAGGAGCAC
CCAGATTTCATAAAGGAAGTCCAGGAATTGAACTCAGCTCTACATCAATCGGACCTAATAGACA
TCTACAGAACTCTCCACCCCGCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTAAAA
A

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FIGURE 3C

SEQ ID NOS:86 and 167

TTTACAATTCTCCTAACACAATGACAAAGAGCAATGAACTAACCCGGGCAGTAGAGGAACTAC
ACAAACTTTTGAAAGAAGCTAGGGAAGATTACAAAGACGATGACGATAAGGCATCCGCTATTT
AAAA

SEQ ID NOS:87 and 168

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGACCTACTGGA
ACCTGCTGCCCCCAAGCGGCCCATCAAAGAGGTGCTGACGGACATCTTTGCCAAGGTGCTGG
AGAAGGGCTGGGTGGACAGCCGCTCCATCCACGATTACAAAGACGATGACGATAAGGCATCCG
CTATTTAAAA

SEQ ID NOS:88 and 169

CTATTTACAATTCTCCTAACACTATGGACTATGAGATGCTCTTCAACTCCTTCAGGGATTACA
AAGACGATGACGATAAGGCATCCGCTATTAAAAA

SEQ ID NOS:89 and 170

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCCGGGGAGG
ACATGGAGATCAGCGTGAAGGAGTTGCGGACAATCCTCAATAGGATCATCAGCAAACACAAAG
ACCTGCGGACCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:90 and 171

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGGACTAAGAG
AAGAAAGTGAAGAGTACATGGCTGCTGCTGATGAATACAATAGACTGAAGCAAGTGAAGCAAC
CTGCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:91 and 172

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGAAGGGCATCA
TCAGCAGGTTGATGTCCGTGGAGGAAGAAGTGAAGAGGGACCACGCAGAGATGCAAGCGGCTG
TGGACTCCAAACAGAAGATCATTGATGCCCAGGAGAAGCGCATTGCCTCGTTGGATGCCGCCA
ATGCCCGCCTCATGAGTGCCCTGACCCAGCTGAAAGAGAGGTACAGCATGCAAGCCCGTAACG
GCATCTCCCCACCAACCCCGCGGATTACAAAGACGATGACGATAAGGCATCCACTATTTAAA
AAA

SEQ ID NOS:92 and 173

TAATACGACTCACTATAGGGACAAATACTATTTACAATTCTCCTAACACAATGTGGGAACGGA
TTGAGGAAAGGCTGGCTTATATTGCTGATCACCTTGGCTTCAGCTGGACAGAATTAGCAAGAG
CGCTGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:93 and 174

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTGCTTACTTCACAATGGCTCGGGG
AGACTTTGCCCAGGCTGCCCAGCAGCTGTGGCTGGCCCTGCGGGCACTGGGCCGGCCCCCTGCC
CACCTCCCACGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:94 and 175

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTCTTTCTCTACAATGGTGGTGGATG
TGCCAGATTTTATAGTCTGGCTTGAGGAGGCAGTATCTGATTTACATAGGGCCCTCGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:95 and 176

CTTTTACAATTCTCCTAACACAATGGGCTTTTTGGCTGCCGAGCAGGACATCCGAGAGGAAAT
CAGAAAAGTTGTACAGAGTTTAGAACAAACAGCTCGAGAGGTTTAACTCTACTGCAAGGGGT
CCAGGATTACAAAGACGATGACGATAAGGCATCCGCTAAGNAAA

SEQ ID NOS:96 and 177

TTAATACGACTCACTATAGGGATTACTATTTACAATTCTTACTTCACAATGCTGGACCCTGTA
AAGGATGTTCTAATTCTTTCTGCTCTGAGACGAATGCTATGGGCTGCAGATGACTTCTTAGAG
GATTTGCCCTTTTGAGCAAATAGGGAATCTAAGGGAGGAAATTATCAACTGTGCACAAGCGGAT
TACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:97 and 178

TTCTATTTACAATTCTCCTAACACAATGGCCAACCTCCTACTCCTCATGGTACCCATTCTAAT
CGCAATGGCATTCTAATGCTTACCGAACGAAAAATTCTAGGCTATATACAACCACGCGATTA
CAAAGACGATGACGATAAGGCATCCGCTAAANAAA

SEQ ID NOS:98 and 179

AATTCTCCTAACACANTGCTCCGGCTAAATACTACCGTATGGCCCACCATAATTACCCCCATA
CTCCTTACACTATTCTCATACCAACCGACTAATCACCACCCGGGATTACAAAGACGATGAC
GATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:99 and 180

CTATTTACAATTCTCCTAACACAATGACCCTCTACCTAAAACTCACAGCCCTCGCTGTCACTT
TCCTAGGACTTCTAACAGCCCTAGACCTCAACTACCCAACCGATTACAAAGACGATGACGATA
AGGCATCCGCTATNAAAAA

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FIGURE 3C

SEQ ID NOS:100 and 181

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGCGGGCGTGT
TCTCAGCCGAGCCGTGCGCGTTTCCACAGACCCGTGCGAGCATGGTGTTTGCCAGGCACCTGC
GGGAGGTGGGAGACGAGTTCAGGAGCAGACATCTCAACTCCACGGACGACGCAGACGAGGATT
ACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:101 and 182

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGGCTTAAAC
TTGCCACAGTTGCTGCCAGTATGGACAGAGTGCCAAAGGTTACTCCCAGCAGTGCCATCAGCA
GCATAGCAAGAGAGAACCACGAACCAGAAAGATTGGGCTTAAATGGAATAGCAGAGACAACAG
ATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:102 and 183

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGATGCGGGATC
TCCCAGGACACTACTATGAAACGCTCAAATTCCTTGTTGGGCCATCTCAAGACCATCGCTGACC
ACCGCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:103 and 184

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTAGGTGTGGATGTGTGG
GGGCCGCATGGAGGACATCCCCTGCTCCAGGGTGGGCCATATCTACAGGAAGTATGTGCCCTA
CAAGGTCCCGCCGGAGTCAGCCTGGCCCCGAACCTTAAGCGGGTGGCCGATTGGATGGATTA
CAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:104 and 185

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCGCTTAGTT
GGATCGAAATGGACACCGAGATGGAGATGCTTCTGGCTAGATTTGCGAGAACCCAGGAGACC
TGCATTTAGACCACTCTGTCCATTTGTGTGCCACCCCGATTACAAAGACGATGACGATAAGG
CATCCGCTATTTAAAA

SEQ ID NOS:105 and 186

CTATTTACAATTCTCCTAACACAATGACCTCCACCCTACCACACATTCTGAAGAACCCGTGATT
ACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:106 and 187

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAACGGAAATC
TGTTGCTTCATTTCATCGCCGACAGTGATTACAAAGACGATGACGATAAGGCATCCGCTATTT
AAAA

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FIGURE 3C

SEQ ID NOS:107 and 188

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCGCCCTGGACGACATCG
AGTGGTTTGTGGCCCCGGCTGCAGAAGGCAGCCGAGGCTTTCAAGCAGCTGAACCAGCCCGAT
TACAAAGACCATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:108 and 189

TAATACGACTCCTATAGGGACAATTACTATTTACAATTCTTACTTCAATACAATGCGCACCCCT
GCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCCTACT
CCAATGGCTCAGACTGCACCCGCTGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTA
AAA

SEQ ID NOS:109 and 190

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACGCCAAAGCACAATGGC
TGTTATAATTAACGAATTATCTCAGCGTGACAGCTGTGGTCCTTTGAAAATTAGCTTGAATAA
CAAGATCCTGGTGTATGGTAATTTATTTCTCTTTACCCCCGATTACAAAGACGATGACGA
TAAGGCATCCGCTATTTAAAA

SEQ ID NOS:110 and 191

CAATTCTCCTAACACGATGGGACTGGCTAAAAAAGTAAAAGGAACCCGGCAAATCTTACCCC
GCCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAAA

SEQ ID NOS:111 and 192

NATTTCTATTTACAATTCTCCTAACACAATGAGCTCACAGGCACTTAGAATCCATCAGTGGCT
CCATCTTTCTCAGACTTCACCTCCACCGATTACAAAGACGATGACGATAAGGCATCCGCTNN
AAAAA

SEQ ID NOS:112 and 193

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGACCAACCCA
TAGGAAAAATGGGAAAAGTTGTTCCCGTTACAACCTTTACAAAACGTTACAAATGCTCATGTCCC
AGATGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:113 and 194

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGGGGTCTCTG
AGGCCGAGGGAACATTTCCGCTCAGCACTTTCTTTCTTGGGATAGCATCCCGTCTAAGAAGCG
TGGCTGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:114 and 195

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAGGGCGCCCA
GATTCATAAAGCAAATATTGCTAGATCTAAAGAGAGAGATAGACTTCAATGTGAGATTAGTAG
AATACTTCAACCCACTATCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:115 and 196

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGATCGTGGCTA
TCATTGCTGGTCGCCTTCGGATGTTGGGTGACCAGTTCAACGGAGAATTGGAAGCTTCTGCCA
AAAACGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:116 and 197

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAACCTGGCTTTGGC
CTATTACAGCAGCCGACAGTATGCTTCAGCACTGAAGCATATCGCTGAGATTATTGAGCGTGG
CATCCGCCAGCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:117 and 198

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACGATGGCTGCCATGT
TATTAGACAGAAGAGGAAGTGTGACCTCTGGATAAATGAGATGTCACTATTACATAAGA
TTGTTCAAGATGTATATGGAACCTCTACCCGCCCCACTCCGATTACAAAGACGATGACGATA
AGGCATCCGCTATTTAAAA

SEQ ID NOS:118 and 199

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGCCTTGGCAAT
ACAAACCGATAGCTGATCTTTACAGAGGGAGAGAGAGCCGTCCCTCTGCCCCCGGGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:119 and 200

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCTGTTCTCAG
TGTTGCTACGTTATTTGGCAGATAACTTTCTGCCAGGAGGATCCGATTACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:120 and 201

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGATTGGCAGG
TGTTGCTAGGAAAACACTTTTGGAATAAGATAATCCGGGCATCGATTACAAAGACGATGACG
ATAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:121 and 202

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGGTGCTATGG
AGAGAGAATGGGCGATGTTTCTCAGGGCTGCTTCAAGCAGGATTAGGGGTGGCGTGGATTACA
AAGACGATGACGATAAGGCATCCGCTGTTTAAAA

SEQ ID NOS:122 and 203

CTATTTACAATTCTCCTAACACAATGGTGCATAACTTTGGGAGACACTGGGGTCTGCCCTTGA
GTTTTCTTCTCAATTACCCTTTATTCTCAGTCCGGATTACAAAGACGATGACGATAAGGCAT
CCGCTATTAAAAA

SEQ ID NOS:123 and 204

TAATACGACTCACTATAGGAAATACTATTTACAATTCTTACTTCACAATGGCTAGCATGGCTC
CAGTGGGGAGAGATGCAGAAACATTGCAAAAGCAAAAGGAACTATAAAAGCCTTTCTAAAGA
AACTAGAAGCCCTCATGGCAAGCAATGACAATGCCAATAAAACCGATGACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:124 and 205

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGTGTGGGAGC
AGGCTGAACTCACTGGGCTCCGCCTGGCAAGCTTGGGGTTGAAGTTTAATAAAATCGTCCATT
CGTCTATGACGCGCGCCATAGAGACCACCGATTACAAAGACGATGACGATAAGGCATCCGCTA
TTTAAAA

SEQ ID NOS:125 and 206

TAATACGACTCACTATAGGGGACAATTACTATTTACAATTCTTACTTCACAATGGGCACTAGA
ATTAGTGATATGCTAAAATTAATTGCAGACACATGGCAGAGAAATTGTTGCCCTGCGGATTAC
AAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:126 and 207

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGGAGCAGGCCA
GTGTTAAGTATGTTATTCTGGATATGTACAGAGCACTCTTGACACTAATGAATACTTCAACAG
CCACAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:127 and 208

CAATTCTCCTAACACAATGGAAGACCTAGAGAGTGTGTTAATAAGACTGATCAACTGGGCAAA
AGGAAGCCCCATCCAGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:128 and 209

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACAATGAGGCCGGTGT
CCTTTTGCAGGGCTGTTTGGACTCTGAACAGGGCAATAGGAAGGCATTTTGTCCGAGGTAGCA
GGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:129 and 210

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCACGCCGTGG
TGGCACGTTTGCCTTACATTGGGGCAATCATGTTCCAACGACTAGACTTCATAGAACAATTGT
CTGCACCCCCAGCGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:130 and 211

CTTTTACAATTCTCCTAACACAATGGGCCAAGGTACACTTTGGGGAAGTGGGATGGAAGCATG
GTTGGCAACGGTGTTGAAGGCACTCCCTTGGCACCCACATACCAGCTGGAGCCGGATTACAA
AGACGATGACGATAAGGCATCCGCTATANAAAA

SEQ ID NOS:131 and 212

TTCTATTTACAATTCTCCTAACACAATGATAGCACAGGCAACGAAAGCAACAATAGACAAATG
GAACTGCATCAAACCTTAAAATCTTCTACACCTCAAAGAAAGAAGCCAGCGATTACAAAGACGA
TGACGATAAGGCATCCGCTANT

SEQ ID NOS:132 and 213

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGTGGTGGATG
TGCCAGATTTTATAGTCTGCTTGAGGAGGCAGTATCTGATTTACATAGAGCCCTCGATTACA
AAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:133 and 214

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGCAGAGGAGAG
GGAATGAATTCCAGCTGAGAGACCTGGCCGATGCATGGGATTTGTCTTCAAGGTCCAGGCAGA
GGGGATGGCAGATGCCAAATTGCAGAAGTCCAAGAGGGCCCCGAGATTACAAAGACGATGACG
ATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:134 and 215

TTTACAATTCTCCTAACACAATGCGGGGCCCTGTGGGTGGACAGGGTCCTAGAGGAATGGGGCC
TGGAACCGCGGCAGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

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FIGURE 3C

SEQ ID NOS:135 and 216

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTACTCTACAATGTTTCGTGAGG
TCTGTTGGCTGGAGGCTGCAGAACATTGGTGATGACATGGACCACGCCATTTGTGGCCATGAT
GTCAGGCTCGGCGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:136 and 217

GCAGTGGACTCAGAAAGCCAACATGTGGCTCCTCCCAGCGCGATTACAAAGACGATGACGATA
AGGCATCCGCTATTTAAAA

SEQ ID NOS:137 and 218

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTTTCTCTACAATGGCGGGTACAC
AGCCACTTATCCTTGCCAGTTTCATGCGTGTGGAGGTGACGAACCTCTCCACTTCCTGCTCT
GGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAA

SEQ ID NOS:138 and 219

TAATACGACTCACTATAGGGACAATTACTATTTACAATTCTCCTAACACCATGATGGATACCA
TAAAGGGATTGACCTAATCACTAATTTTCAGGTGGTGGCTGATGCTTTGAACATCTCTTTGC
TGCCCAATCCATTAGCGACAGCGGATTACAAAGACGATGACGATAAGGCATACGCTATTTAAA
A

SEQ ID NOS:139 and 220

TCTATTTACAATTCTCCTAACACAATGGCCACTTGGATGAAAACCCTTCAAGGATTACTGGAT
AGAATTCAGGCTTTCCCTCCAGCCCCACGATTACAAAGACGATGACGATAAGGCATCCGCT
ANGAAAAAA

SEQ ID NOS:140 and 221

CTATTTACAATTCTCCTAACACAATGGAAGCTAATAGAAAACAACCGAAACCAATAATTCAA
GCACTGCTTATTACAATTTTACTGGGGTCTCTATTTTACCCTCCTACAAGCCCCAGATTACAA
AGACGATGACGATAAGGCATCCGCTATAAAAAA

SEQ ID NOS:141 and 222

TTCTATTTACAATTCTCCTAACACAATGGGGCTCACTCACCACCATTAACAACATAAAAC
CCTCATCCACACGAGATTACAAAGACGATGACGATAAGGCATCCGCTANAAAAA

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FIGURE 3C

SEQ ID NOS:142 and 223

TAATACGACTCATATAGGGACAATTACTATTTACAATTCTTACTTCACAATGGTGAGCTGCTG
GCCGATTACTAAAATACCCTTTGTCTACAGCCTCCGCTTCTCTCCTGGCTACGCAATTGAAA
GCATAGCGGATTACAAAGACGATGACGATAAGGCATCCGCTATTTAAAAAA

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A. BimL

10 20 30 40 50 60 70 80 90 100 110 120 130
MAKQPSVSECDREGQLOPAERPPQLRPGAPTSLOTEPQDRSPAPMSCDKSTQTPSPCCQAFNHVLSAMASMRQAEPADMRPRMTIAQELRRICGFENAYYARRVFLNNYQAAEDHPRVTLRLRYIVRLWFMH
1 P57-V107
1 A72-H118
3 -A115
1 -A114
16 -V107
20 -R106
7 R75-S120*
2 -P199*
1 -H118
1 -A115
4 -V107
9 -R106
5 Q76-R106

B. Bax

10 20 30 40 50 60 70 80 90 100 110 120 210
MDGSGEPGGGTSSEIQIMKYGALLQGTQDRAGMNGEAPELADPTQDAKYKLSCLKRIQDELDNMLQRMIAAVDTSPREVFVRADMFSDGNFNGRVVALFYFASKVLKA // DVYINAFSLRY
1 G39-M86*
1 -R89
1 -D84
1 -V83
1 -A82
1 -Q77
1 D48-R89
1 -V83
13 K58-H118

C. HSPC300

10 20 30 40 50 60 70 80 90 100
MGAAMAGQEDPVQREXHOEWANREYIEITTSIKKIADFLNSFDMSCRSRLATNEKLTALERRIEYIEARYTKGETLTRTPCCQCEVALHNTGHMGKAPAFSFLSP
11 G2-F43
6 -S42
13 A6-F43
4 -S42

D. TPR

10 280 290 300 310 320 330 340 350 360 370 2340
MAAVLQQVLE // NAHIKLSNLYKSAADDSKSNELTRAVEELHKLKEAGEANKAIQDHLLVEQSKDQWEREMLEKIGLEKELNANDLLSATKKGALLSEELAAMSPT // RGINRGMIN
19 D294-P322*
2 A298-E319

FIGURE 4

20200505/2600F

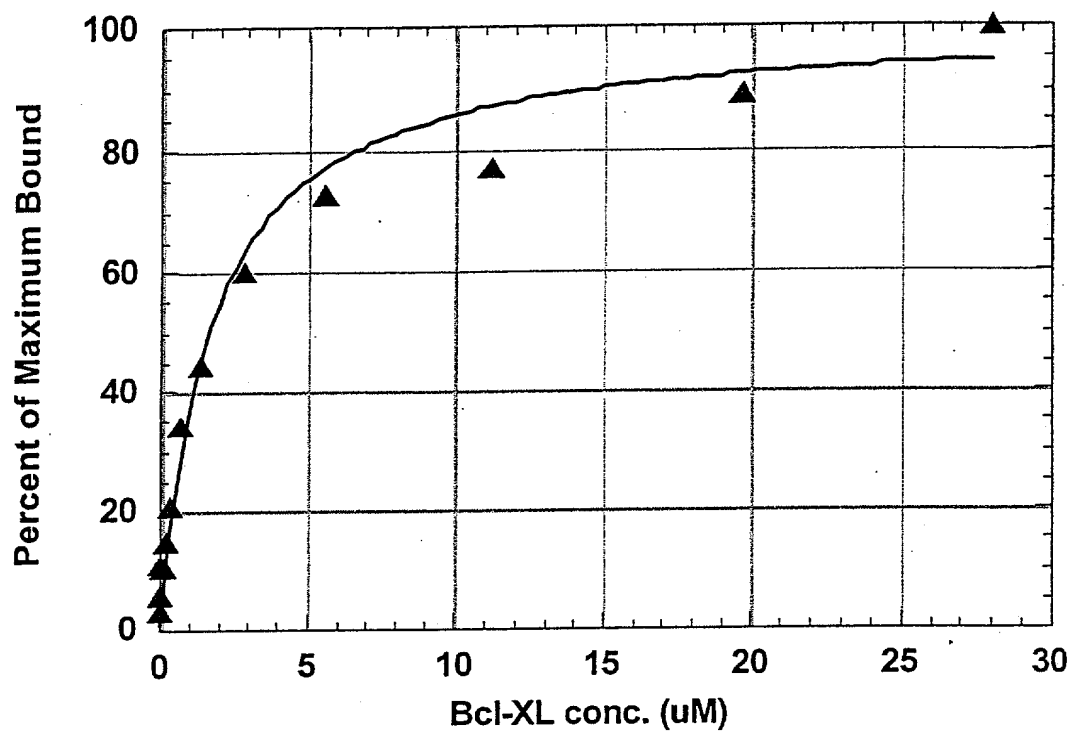


FIGURE 5

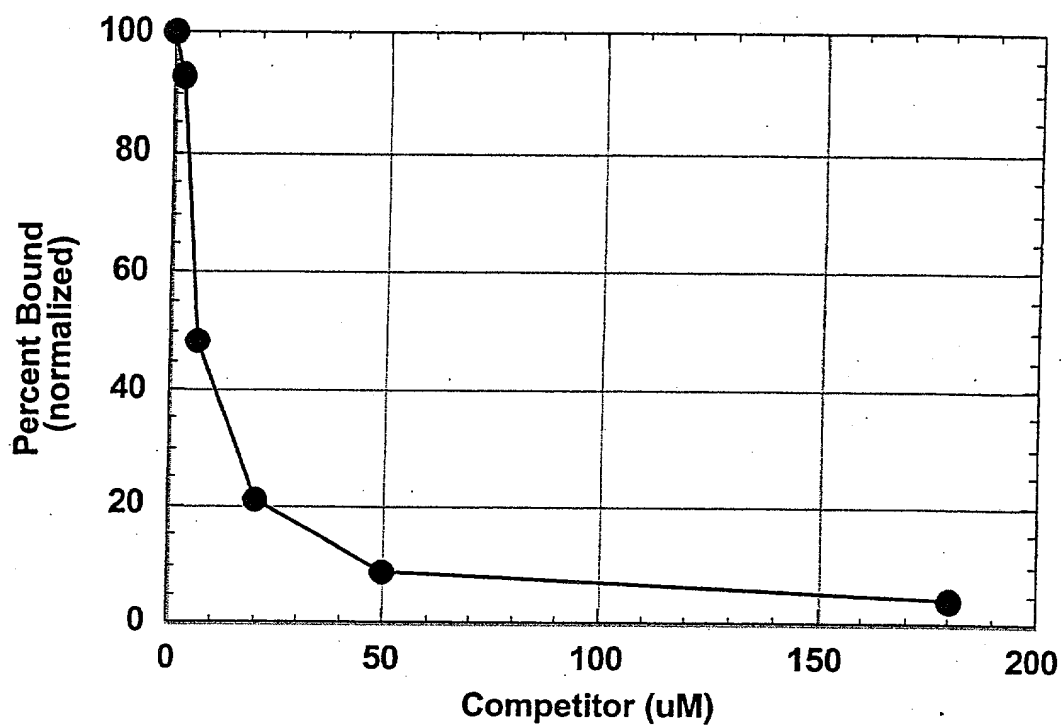


FIGURE 6

Clone ID	Protein	Competed Binding	Selected sequence (note that each peptide was preceded by an initiator methionine and followed by the sequence DYKDDDDKASA)
T44	Bim	0.84	PEIWAQEEERERERENAYYARR
T95	Neutrophil Cyto. factor	0.66	Q R G M L Y Y Q T E K Y D L A K K D - D E A L I Q L R G N N
V47	Hypothetical protein	0.36	R W W M C G G R M E D M C C R V G H
C21	Novel protein I	0.44	AAQATKATIKKNCIKLKIFYTSKKKEAS
V18	Novel protein A	0.37	VVDVDPFVWLEEAASDLHRAI
X56	Talin	0.21	GGESDTPHFDAMQLAKAAASAAALVLKAKSVAAQR
V72	unknown protein	0.2	A A M L L D R R G T E C D L W I N E M S L L H K I Q Q V G T P H P P H S
c32	Bak	0.36	G Q G R Q Q A I G G D D N R R K
Y37	unknown protein	ND	A L S W I E M D T E M E M L L A R F R T P T P D L H L D H S V H L C A H P
Y75	Bcl-2 related protein BPR	ND	T G K E A I L R R L V A L L E E E A E V I N Q K L A S D P A L R S K L L S S S F A H L
V06	Golgi SNAP receptor	0.12	G T R Q D R M F E T M A I E I E Q Q L A R T G N N K M A E Y T
C68	HSPC300	0.21	A V Q E D P V Q R E I H Q D W A N R E Y I E I T S S K K K K
U58	Syntaxin 4A	0.14	A T R Q A L N E I S A R H S G I Q Q L E R S T E E H D I E T F L
V50	Tumor protein	0.18	M F S D I Y G R E E E A D G G C L E V E G K M V S R P E
C49	Bax	0.06	K A S E C E K K K G D E D S N M E L Q R M I A A V D T D S P R
U15	Toll-like R3	0.07	F W L E E R D F E A G V F E L E A V N S K K S
Y01	Unknown protein	0.08	L S V L E R Y K K K N E L P G G S
W06	Anion Channel	0.32	M K W D T D N T L G T E I S W E N K K A E G K L T L D T F V H H V L H A P H
V68	Novel B	0.9	C R E Q A E L T G L R L A S L G L K F N K I V H S S M T R A I E T
T25	Novel D	0.26	G T R I S D M K K L A D T Q R N C C P A

FIGURE 7

Number	Protein Name	Accession number	Clone	Protein Sequence
224	Cdc21	CAA52801	AtB-Br-M39	KYQQLFEDIRW
225	SRP9	NP_003124	AtB-Hc-6	IGEEFSRAAEKLYLAV
226	Bmf	NP_277038	AtB-Thy-34	KAEVQIARKLQCIADQFHRLHVL
227	Unknown protein from human chromosome 2 clone RP11-228G11	AC098559	AtB-Br-M45	MGDVVGFIDELEGAVSDLHRAL
228	Unknown protein from human chromosome 14 clone CTD-3014H8 and RP11-285P	AC007955	AtB-Thy-38	TLRHWGLQFNTRFGV
229	Sequence/protein not in database	none	AtB-BM-51	SRREEAWDALFRGI
230	Sequence/protein not in database	none	AtB-BM-52	TLREIGDLYLTSILGRR

Figure 8A

20200905225007

SEQ ID NO: 224 Cdc21 (Corresponds to nucleic acid sequence of SEQ ID NO: 231)

KYQQLFEDIRW

SEQ ID NO: 225 SRP9 (Corresponds to nucleic acid sequence of SEQ ID NO: 232)

IGEEFSRAAEKLYLAV

SEQ ID NO: 226 Bmf (Corresponds to nucleic acid sequence of SEQ ID NO: 233)

KAEVQIARKLQCIADQFHRLHVL

SEQ ID NO: 227 Unknown protein from human chromosome 2 clone RP11-228G11 (Corresponds to nucleic acid sequence of SEQ ID NO: 234)

MGDVVGFIDELEGAVSDLHRAL

SEQ ID NO: 228 Unknown protein from human chromosome 14 clone CTD-3014H8 and RP11-285P (Corresponds to nucleic acid sequence of SEQ ID NO: 235)

TLRHWGLQFNTRFGV

SEQ ID NO: 229 Sequence/protein not in database (Corresponds to nucleic acid sequence of SEQ ID NO: 236)

SRREEAWDALFRGI

SEQ ID NO: 230 Sequence/protein not in database (Corresponds to nucleic acid sequence of SEQ ID NO: 237)

TLREIGDLYLTSILGRR

Figure 8B

SEQ ID NO: 231

AAATACCAGCAACTTTTTGAAGATATTCGGTGG

SEQ ID NO: 232

ATCGGGGAGGAGTTCAGCCGCGCTGCCGAGAAGCTTTACCTCGCTGTT

SEQ ID NO: 233

AAAGCAGAGGTACAGATTGCCCCGAAAGCTTCAGTGCATTGCAGACCAAGTTC
CACCGGCTTCATGTGCTT

SEQ ID NO: 234

ATGGGAGATGTGGTTGGTTTTATAGACGAACTTGAGGGGGCAGTGTCTGAT
TTACATAGGGCGTTG

SEQ ID NO: 235

ACACTCCGACACTGGGGATTACAGTTCAACACAAGATTTGGTGTG

SEQ ID NO: 236

TCGAGAAGGGAAGAGGCATGGGATGCTTTATTTTCGTGGGATC

SEQ ID NO: 237

TCGAGAAGGGAAGAGGCATGGGATGCTTTATTTTCGTGGGATC

Figure 8c

2040E0.052600T

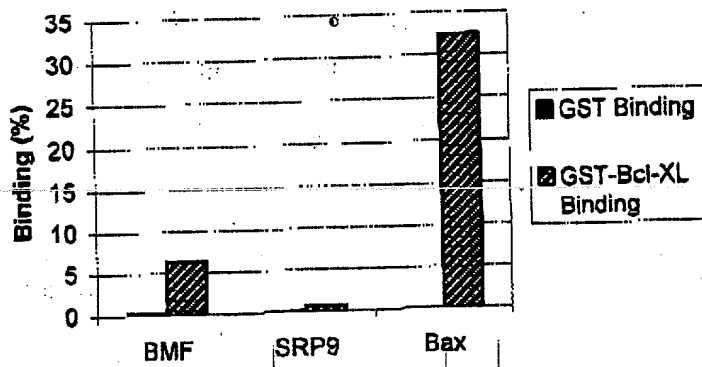


Figure 9

SRP9

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SRP9

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to